

<110> Trotta, Christopher R.

<130> 10589-034-999

<140> US/10/551,300

<141> 2005-09-27

<150> PCT/US2004/009590

<151> 2004-03-26

<150> 60/458,067

<151> 2003-03-27

<160> 4

<170> FastSEQ for Windows Version 4.0

 $\langle 210 \rangle$ 1

<211> 465

<212> PRT

<213> Homo sapiens

<220>

<223> HsSen2p

<400> 1

1

Gln Asp Ala Leu Ile Leu Gln Arg Gly Leu His His Glu Asp Gly Ser
 225 230 235 240
 Gln His Ile Gly Leu Leu His Pro Gly Asp Arg Gly Pro Asp His Glu
 245 250 255
 Tyr Val Leu Val Glu Glu Ala Glu Cys Ala Met Ser Glu Arg Glu Ala
 260 265 270
 Ala Pro Asn Glu Glu Leu Val Gln Arg Asn Arg Leu Ile Cys Arg Arg
 275 280 285
 Asn Pro Tyr Arg Ile Phe Glu Tyr Leu Gln Leu Ser Leu Glu Glu Ala
 290 295 300
 Phe Phe Leu Val Tyr Ala Leu Gly Cys Leu Ser Ile Tyr Tyr Glu Lys
 305 310 315 320
 Glu Pro Leu Thr Ile Val Lys Leu Trp Lys Ala Phe Thr Val Val Gln
 325 330 335
 Pro Thr Phe Arg Thr Thr Tyr Met Ala Tyr His Tyr Phe Arg Ser Lys
 340 345 350
 Gly Trp Val Pro Lys Val Gly Leu Lys Tyr Gly Thr Asp Leu Leu Leu
 355 360 365
 Tyr Arg Lys Gly Pro Pro Phe Tyr His Ala Ser Tyr Ser Val Ile Ile
 370 375 380
 Glu Leu Val Asp Asp His Phe Glu Gly Ser Leu Arg Arg Pro Leu Ser
 385 390 395 400
 Trp Lys Ser Leu Ala Ala Leu Ser Arg Val Ser Val Asn Val Ser Lys
 405 410 415
 Glu Leu Met Leu Cys Tyr Leu Ile Lys Pro Ser Thr Met Thr Asp Lys
 420 425 430
 Glu Met Glu Ser Pro Glu Cys Met Lys Arg Ile Lys Val Gln Glu Val
 435 440 445
 Ile Leu Ser Arg Trp Val Ser Ser Arg Glu Arg Ser Asp Gln Asp Asp
 450 455 460
 Leu
 465

<210> 2
 <211> 448
 <212> PRT
 <213> Homo sapiens

<220>
 <223> HsSen2 variant

<400> 2
 Met Ala Glu Ala Val Phe His Ala Pro Lys Arg Lys Arg Arg Val Tyr
 1 5 10 15
 Glu Thr Tyr Glu Ser Pro Leu Pro Ile Pro Phe Gly Gln Asp His Gly
 20 25 30
 Pro Leu Lys Glu Phe Lys Ile Phe Arg Ala Glu Met Ile Asn Asn Asn
 35 40 45
 Val Ile Val Arg Asn Ala Glu Asp Ile Glu Gln Leu Tyr Gly Lys Gly
 50 55 60
 Tyr Phe Gly Lys Gly Ile Leu Ser Arg Ser Arg Pro Ser Phe Thr Ile
 65 70 75 80
 Ser Asp Pro Lys Leu Val Ala Lys Trp Lys Asp Met Lys Thr Asn Met
 85 90 95
 Pro Ile Ile Thr Ser Lys Arg Tyr Gln His Ser Val Glu Trp Ala Ala
 100 105 110
 Glu Leu Met Arg Arg Gln Gly Gln Asp Glu Ser Thr Val Arg Arg Ile
 115 120 125
 Leu Lys Asp Tyr Thr Lys Pro Leu Glu His Pro Pro Val Lys Arg Asn
 130 135 140

Glu	Glu	Ala	Gln	Val	His	Asp	Lys	Leu	Asn	Ser	Gly	Met	Val	Ser	Asn	
145					150					155					160	
Met	Glu	Gly	Thr	Ala	Gly	Gly	Glu	Arg	Pro	Ser	Val	Val	Asn	Gly	Asp	
				165					170						175	
Ser	Gly	Lys	Ser	Gly	Gly	Val	Gly	Asp	Pro	Arg	Glu	Pro	Leu	Gly	Cys	
			180					185					190			
Leu	Gln	Glu	Gly	Ser	Gly	Cys	His	Pro	Thr	Thr	Glu	Ser	Phe	Glu	Lys	
			195				200					205				
Ser	Val	Arg	Glu	Asp	Ala	Ser	Pro	Leu	Pro	His	Val	Cys	Cys	Cys	Lys	
	210					215					220					
Gln	Asp	Ala	Leu	Ile	Leu	Gln	Arg	Gly	Leu	His	His	Glu	Asp	Gly	Ser	
225					230					235					240	
Gln	His	Ile	Gly	Leu	Leu	His	Pro	Gly	Asp	Arg	Gly	Pro	Asp	His	Glu	
				245					250					255		
Tyr	Val	Leu	Val	Glu	Glu	Ala	Glu	Cys	Ala	Met	Ser	Glu	Arg	Glu	Ala	
			260					265					270			
Ala	Pro	Asn	Glu	Glu	Leu	Val	Gln	Arg	Asn	Arg	Leu	Ile	Cys	Arg	Arg	
		275					280					285				
Asn	Pro	Tyr	Arg	Ile	Phe	Glu	Tyr	Leu	Gln	Leu	Ser	Leu	Glu	Glu	Glu	
	290					295					300					
Pro	Leu	Thr	Ile	Val	Lys	Leu	Trp	Lys	Ala	Phe	Thr	Val	Val	Gln	Pro	
305					310					315					320	
Thr	Phe	Arg	Thr	Thr	Tyr	Met	Ala	Tyr	His	Tyr	Phe	Arg	Ser	Lys	Gly	
				325					330					335		
Trp	Val	Pro	Lys	Val	Gly	Leu	Lys	Tyr	Gly	Thr	Asp	Leu	Leu	Leu	Tyr	
			340					345					350			
Arg	Lys	Gly	Pro	Pro	Phe	Tyr	His	Ala	Ser	Tyr	Ser	Val	Ile	Ile	Glu	
		355					360					365				
Leu	Val	Asp	Asp	His	Phe	Glu	Gly	Ser	Leu	Arg	Arg	Pro	Leu	Ser	Trp	
		370				375					380					
Lys	Ser	Leu	Ala	Ala	Leu	Ser	Arg	Val	Ser	Val	Asn	Val	Ser	Lys	Glu	
385					390					395					400	
Leu	Met	Leu	Cys	Tyr	Leu	Ile	Lys	Pro	Ser	Thr	Met	Thr	Asp	Lys	Glu	
				405					410					415		
Met	Glu	Ser	Pro	Glu	Cys	Met	Lys	Arg	Ile	Lys	Val	Gln	Glu	Val	Ile	
			420					425					430			
Leu	Ser	Arg	Trp	Val	Ser	Ser	Arg	Glu	Arg	Ser	Asp	Gln	Asp	Asp	Leu	
		435					440					445				

<210> 3
 <211> 377
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<220>
 <223> Sc Sen2p

<400> 3
 Met Ser Lys Gly Arg Val Asn Gln Lys Arg Tyr Lys Tyr Pro Leu Pro
 1 5 10 15
 Ile His Pro Val Asp Asp Leu Pro Glu Leu Ile Leu His Asn Pro Leu
 20 25 30
 Ser Trp Leu Tyr Trp Ala Tyr Arg Tyr Tyr Lys Ser Thr Asn Ala Leu
 35 40 45
 Asn Asp Lys Val His Val Asp Phe Ile Gly Asp Thr Thr Leu His Ile
 50 55 60
 Thr Val Gln Asp Asp Lys Gln Met Leu Tyr Leu Trp Asn Asn Gly Phe
 65 70 75 80
 Phe Gly Thr Gly Gln Phe Ser Arg Ser Glu Pro Thr Trp Lys Ala Arg
 85 90 95

Thr	Glu	Ala	Arg	Leu	Gly	Leu	Asn	Asp	Thr	Pro	Leu	His	Asn	Arg	Gly	
			100					105					110			
Gly	Thr	Lys	Ser	Asn	Thr	Glu	Thr	Glu	Met	Thr	Leu	Glu	Lys	Val	Thr	
		115					120					125				
Gln	Gln	Arg	Arg	Leu	Gln	Arg	Leu	Glu	Phe	Lys	Lys	Glu	Arg	Ala	Lys	
		130				135					140					
Leu	Glu	Arg	Glu	Leu	Leu	Glu	Leu	Arg	Lys	Lys	Gly	Gly	His	Ile	Asp	
145					150					155					160	
Glu	Glu	Asn	Ile	Leu	Leu	Glu	Lys	Gln	Arg	Glu	Ser	Leu	Arg	Lys	Phe	
			165				170							175		
Lys	Leu	Lys	Gln	Thr	Glu	Asp	Val	Gly	Ile	Val	Ala	Gln	Gln	Gln	Asp	
			180					185					190			
Ile	Ser	Glu	Ser	Asn	Leu	Arg	Asp	Glu	Asp	Asn	Asn	Leu	Leu	Asp	Glu	
		195					200					205				
Asn	Gly	Asp	Leu	Leu	Pro	Leu	Glu	Ser	Leu	Glu	Leu	Met	Pro	Val	Glu	
		210				215					220					
Ala	Met	Phe	Leu	Thr	Phe	Ala	Leu	Pro	Val	Leu	Asp	Ile	Ser	Pro	Ala	
225					230					235					240	
Cys	Leu	Ala	Gly	Lys	Leu	Phe	Gln	Phe	Asp	Ala	Lys	Tyr	Lys	Asp	Ile	
			245					250						255		
His	Ser	Phe	Val	Arg	Ser	Tyr	Val	Ile	Tyr	His	His	Tyr	Arg	Ser	His	
			260					265					270			
Gly	Trp	Cys	Val	Arg	Ser	Gly	Ile	Lys	Phe	Gly	Cys	Asp	Tyr	Leu	Leu	
		275					280					285				
Tyr	Lys	Arg	Gly	Pro	Pro	Phe	Gln	His	Ala	Glu	Phe	Cys	Val	Met	Gly	
		290				295					300					
Leu	Asp	His	Asp	Val	Ser	Lys	Asp	Tyr	Thr	Trp	Tyr	Ser	Ser	Ile	Ala	
305					310					315					320	
Arg	Val	Val	Gly	Gly	Ala	Lys	Lys	Thr	Phe	Val	Leu	Cys	Tyr	Val	Glu	
			325					330						335		
Arg	Leu	Ile	Ser	Glu	Gln	Glu	Ala	Ile	Ala	Leu	Trp	Lys	Ser	Asn	Asn	
			340				345						350			
Phe	Thr	Lys	Leu	Phe	Asn	Ser	Phe	Gln	Val	Gly	Glu	Val	Leu	Tyr	Lys	
		355					360					365				
Arg	Trp	Val	Pro	Gly	Arg	Asn	Arg	Asp								
		370				375										

<210> 4

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Motif of the active site for the 5' splice site of yeast
and archael tRNA splicing endonuclease

<400> 4

Tyr	Arg	Gly	Gly	Tyr
1				5